

PTO/PCT Rec'd 09 AUG 2002

PATENT #4.

## IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of:  
Irina Caminschi, et al.

Serial No.: 10/070,982

Filed: March 8, 2002

For: DENDRITIC CELL MEMBRANE  
PROTEIN FIRE

Group Art Unit: Unknown

Examiner: Unknown

Atty. Dkt. No.: FBRC:011US

## EXPRESS MAIL MAILING LABEL

NUMBER EL 839265725 US

DATE OF DEPOSIT August 9, 2002

**SECOND PRELIMINARY AMENDMENT****BOX PCT**

Commissioner for Patents  
Washington, D.C. 20231

Sir:

Please amend the above-identified patent application as follows:

**AMENDMENT****In the specification:**

Please insert as the first paragraph of the specification the following paragraph:

This is a U.S. National Application under 35 U.S.C. § 371 of International Application  
No. PCT/AU00/01083 filed on September 11, 2000, which claims the benefit of priority to AU  
PQ 2728 filed on September 9, 1999.

**In the claims:**

Please amend claim 1 as follows:

10/16/2002 SANDED1 00000006 10070982

01 FC:1615

486.00 0P

1. An isolated polypeptide comprising the amino acid sequence of SEQ ID NO:1 or a functional fragment thereof or an amino acid sequence having at least 50% identity to the amino acid sequence of SEQ ID NO:1 or a functional fragment thereof.

Please add the following new claims:

27. (New) The isolated polypeptide of claim 1, wherein the amino acid sequence has at least 50% identity to the amino acid sequence of SEQ ID NO: 1.
28. (New) The isolated polypeptide of claim 27, wherein the amino acid sequence has at least 70% identity to the amino acid sequence of SEQ ID NO: 1.
29. (New) The isolated polypeptide of claim 27, wherein the amino acid sequence has at least 80% identity to the amino acid sequence of SEQ ID NO: 1.
30. (New) The isolated polypeptide of claim 27, wherein the amino acid sequence has at least 90% identity to the amino acid sequence of SEQ ID NO: 1.
31. (New) An isolated polypeptide comprising the amino acid sequence of SEQ ID NO:2 or a functional fragment thereof or an amino acid sequence having at least 50% identity to the amino acid sequence of SEQ ID NO:2 or a functional fragment thereof.
32. (New) The isolated polypeptide of claim 31, wherein the amino acid sequence has at least 50% identity to the amino acid sequence of SEQ ID NO: 2.
33. (New) The isolated polypeptide of claim 32, wherein the amino acid sequence has at least 70% identity to the amino acid sequence of SEQ ID NO: 2.
34. (New) The isolated polypeptide of claim 32, wherein the amino acid sequence has at least 80% identity to the amino acid sequence of SEQ ID NO: 2.
35. (New) The isolated polypeptide of claim 32, wherein the amino acid sequence has at least 90% identity to the amino acid sequence of SEQ ID NO: 2.

36. (New) An isolated ligand, wherein the ligand interacts with a functional fragment of SEQ ID NO: 1 or SEQ ID NO: 2.
37. (New) The isolated ligand of claim 36, wherein the functional fragment has at least 50% identity to the amino acid sequence of SEQ ID NO: 1 or SEQ ID NO: 2.
38. (New) The isolated ligand of claim 36, wherein the functional fragment has at least 70% identity to the amino acid sequence of SEQ ID NO: 1 or SEQ ID NO: 2.
39. (New) The isolated ligand of claim 36, wherein the functional fragment has at least 80% identity to the amino acid sequence of SEQ ID NO: 1 or SEQ ID NO: 2.
40. (New) The isolated ligand of claim 36, wherein the functional fragment has at least 90% identity to the amino acid sequence of SEQ ID NO: 1 or SEQ ID NO: 2.
41. (New) The isolated ligand of claim 36, wherein the functional fragment has the amino acid sequence of SEQ ID NO: 1 or SEQ ID NO: 2.
42. (New) The isolated ligand of claim 36, wherein the ligand is an antibody.
43. (New) The isolated ligand of claim 42, wherein the ligand is the binding portion of the antibody.
44. (New) An isolated nucleic acid molecule comprising the sequence of SEQ ID NO:3, a sequence having at least 60% identity to the sequence of SEQ ID NO:3, a sequence which hybridizes to the sequence of SEQ ID NO:3 under stringent conditions, or a sequence encoding a functional analogue of a polypeptide of SEQ ID NO:1.
45. (New) The isolated nucleic acid molecule of claim 44, wherein the nucleic acid molecule comprises a sequence of at least 60% identity with the sequence of SEQ ID NO:3.
46. (New) The isolated nucleic acid molecule of claim 45, wherein the nucleic acid molecule comprises a sequence of at least 70% identity with the sequence of SEQ ID NO:3.
47. (New) The isolated nucleic acid molecule of claim 45, wherein the nucleic acid molecule comprises a sequence of at least 80% identity with the sequence of SEQ ID NO:3.

48. (New) The isolated nucleic acid molecule of claim 45, wherein the nucleic acid molecule comprises a sequence of at least 90% identity with the sequence of SEQ ID NO:3.
49. (New) An isolated nucleic acid molecule comprising the sequence of SEQ ID NO:4, a sequence having at least 60% identity to the sequence of SEQ ID NO:4, a sequence which hybridizes to the sequence of SEQ ID NO:4 under stringent conditions, or a sequence encoding a functional analogue of a polypeptide of SEQ ID NO:2.
50. (New) The isolated nucleic acid molecule of claim 49, wherein the nucleic acid molecule comprises a sequence of at least 60% identity with the sequence of SEQ ID NO:4.
51. (New) The isolated nucleic acid molecule of claim 50, wherein the nucleic acid molecule comprises a sequence of at least 70% identity with the sequence of SEQ ID NO:4.
52. (New) The isolated nucleic acid molecule of claim 50, wherein the nucleic acid molecule comprises a sequence of at least 80% identity with the sequence of SEQ ID NO:4.
53. (New) The isolated nucleic acid molecule of claim 50, wherein the nucleic acid molecule comprises a sequence of at least 90% identity with the sequence of SEQ ID NO:4.
54. (New) An isolated nucleic acid molecule encoding the binding region of a ligand, wherein the ligand interacts with a functional fragment of SEQ ID NO: 1 or SEQ ID NO: 2.
55. (New) The isolated nucleic acid molecule of claim 54, wherein the ligand is an antibody.
56. (New) A composition for use in raising or lowering an immune response in a subject comprising a ligand that interacts with a functional fragment of SEQ ID NO: 1 or SEQ ID NO: 2 and an antigen.
57. (New) The composition of claim 56, further comprising a carrier.
58. (New) The composition of claim 56, further comprising an adjuvant.
59. (New) The composition of claim 56, further comprising an adjuvant and a carrier.
60. (New) The composition of claim 56, wherein the antigen is associated with the ligand.

61. (New) The composition of claim 56, wherein the antigen is conjugated to the ligand.
62. (New) A composition for use in raising or lowering an immune response in a subject comprising a nucleic acid molecule and a carrier, wherein the nucleic acid molecule comprises a first sequence encoding a ligand that interacts with a functional fragment of SEQ ID NO: 1 or SEQ ID NO: 2 and a second sequence encoding an antigen.
63. (New) A method of screening a putative compound for immunological regulatory activity comprising:
  - (a) reacting the compound with a polypeptide comprising the amino acid sequence of SEQ ID NO:1 or a functional fragment thereof or an amino acid sequence having at least 50% identity to the amino acid sequence of SEQ ID NO:1 or a functional fragment thereof; and
  - (b) measuring the interaction between the compound and the polypeptide.
64. (New) A method of isolating an antigen presenting cell from a biological sample comprising contacting the biological sample with a ligand, wherein the ligand interacts with a functional fragment of SEQ ID NO: 1 or SEQ ID NO: 2, to form a complex between the ligand and the antigen presenting cell and isolating the complex formed between the ligand and the antigen presenting cell from the biological sample.
65. (New) The method of claim 64, wherein the ligand is immobilized on a solid support.
66. (New) A method of immunizing a subject comprising:
  - (a) isolating antigen presenting cells from a fluid sample obtained from the subject, wherein the isolation involves contacting the fluid sample with a ligand that interacts with a functional fragment of SEQ ID NO: 1 or SEQ ID NO: 2;
  - (b) exposing the cells isolated from step (a) to an antigen; and
  - (c) reintroducing the cells from step (b) into the subject.

67. (New) The method of claim 66, further comprising the step of growing the antigen presenting cells *in vitro* after step (a).
68. A method of immunizing a subject comprising:
  - (a) obtaining a fluid sample from the subject;
  - (b) isolating precursor cells from the fluid sample by contacting the fluid sample with a ligand that interacts with a functional fragment of SEQ ID NO: 1 or SEQ ID NO: 2;
  - (c) growing the cells isolated from step (a) *in vitro* such that they mature and differentiate to become antigen presenting cells;
  - (d) exposing the cells obtained in step (c) to an antigen; and
  - (e) reintroducing the cells from step (d) into the subject.
69. (New) A method of modulating an immune response in a subject comprising administering to the subject a ligand that interacts with a functional fragment of SEQ ID NO: 1 or SEQ ID NO: 2 such that the ligand binds to and inhibits the function of an antigen presenting cell.
70. (New) The method of claim 69, wherein the antigen presenting cell is a myeloid dendritic cell.
71. (New) The method of claim 69, further comprising the step of administering an antigen to the subject.
72. (New) The method of claim 71, wherein the antigen is administered after administration of the ligand.

**REMARKS**

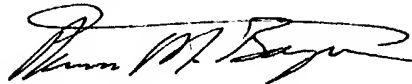
**I. State of the claims**

Claims 1-26 were present in the PCT application and were filed with the application on March 8, 2002. Claims 2-26 were cancelled without prejudice or disclaimer in a First Preliminary Amendment filed concurrently with the application. Applicants expressly reserved the right to pursue claims to the subject matter of claims 2-26. Applicants add by the present amendment claims 27-72. Therefore, claims 1 and 27-72 are currently pending. No new matter is introduced by these amendments.

**II. Conclusion**

Examination of the amended claims is respectfully requested.

Respectfully submitted,



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Attorney for Applicants

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Date: August 9, 2002

10/070982

JC13 Rec'd PCT/PTO 08 MAR 2002

Express Mail Cert. No. EL794535315US  
Date: March 8, 2002

PATENT

**IN THE UNITED STATES PATENT AND TRADEMARK OFFICE  
DO/EO/US RECEIVING OFFICE**

Applicants for DO/EO/US:

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VANDENABEELE, Mark Dexter WRIGHT,  
Kenneth Douglas SHORTMAN

Atty. Dkt. No.: FBRC:011/TMB

International Application No.: PCT/AU00/01083

International Filing Date: 11 September 2000

Title: DENDRITIC CELL MEMBRANE PROTEIN  
FIRE

**PRELIMINARY AMENDMENT**

**BOX PCT**

Assistant Commissioner for Patents  
Washington, D.C. 20231

Sir:

Please amend the above-identified patent application as follows:

**AMENDMENT**

**In the claims:**

Please cancel without prejudice or disclaimer claims 2-26.



## **REMARKS**

### **I. State of the claims**

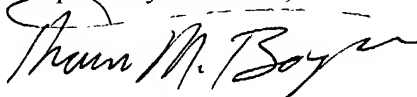
Claims 1-26 were present in the PCT application and were filed herewith. Claims 2-26 have been cancelled without prejudice or disclaimer. Applicants expressly reserve the right to pursue claims to the subject matter of claims 2-26.

### **II. Conclusion**

The claims have been amended to eliminate multiple dependencies. Examination of the amended claim is respectfully requested.

No fees are believed to be due in connection with the filing of this Preliminary Amendment; however, should any fees under 37 C.F.R. §§ 1.16 to 1.21 be deemed necessary for any reason relating to the enclosed materials, the Commissioner is hereby authorized to deduct said fees from Fulbright & Jaworski Deposit Account No. 50-1212/10011874/TMB.

Respectfully submitted,



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Attorney for Applicants

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600 Congress Avenue, Suite 2400  
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(512) 536-3043

Date: March 8, 2002

## SEQUENCE LISTING

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<212> DNA

<213> Homo sapiens

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 gaagatatta atgaatgtga aaccgggctg gcaaagtgca agtataaagc atattgtagg 180  
 aataaagggtg gaggttacat ctgtagctgt ttggtaaaat atactttatt caactttctg 240  
 gctgggtatta tagattatga tcatccggat tgttacgaga acaatagtca agggacgaca 300  
 cagtcaaaacg tggatatttg ggaaaatctg agaagaaatg gaagcagaga ggactttgca 360  
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 tgtggagaaa taggaacact tttacactgt tgggtgggact gtaaaactagt tcaaccatcg 2460





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 225 230 235 240  
 Ser Tyr Phe Cys Thr Cys His Pro Gly Phe Ala Pro Ser Ser Gly Gln  
 245 250 255  
 Leu Asn Phe Thr Asp Gln Gly Val Glu Cys Arg Asp Ile Asp Glu Cys  
 260 265 270  
 Arg Gln Asp Pro Ser Thr Cys Gly Pro Asn Ser Ile Cys Thr Asn Ala  
 275 280 285  
 Leu Gly Ser Tyr Ser Cys Gly Cys Ile Val Gly Phe His Pro Asn Pro  
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 Glu Gly Ser Gln Lys Asp Gly Asn Phe Ser Cys Gln Arg Val Leu Phe  
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 Lys Cys Lys Glu Asp Val Ile Pro Asp Asn Lys Gln Ile Gln Gln Cys  
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 Gln Glu Gly Thr Ala Val Lys Pro Ala Tyr Val Ser Phe Cys Ala Gln  
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 355 360 365  
 Thr Val Val Ser Leu Lys Asn Thr Thr Glu Ser Phe Val Pro Val Leu  
 370 375 380  
 Lys Gln Ile Ser Met Trp Thr Lys Phe Thr Lys Glu Glu Thr Ser Ser  
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 405 410 415  
 Phe Trp Lys Pro Ser Ala Asn Val Thr Pro Ala Val Arg Ala Glu Tyr  
 420 425 430  
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 Val Thr Leu Asp Leu Val Ala Lys Gly Asp Lys Met Lys Ile Gly Cys  
 450 455 460  
 Ser Thr Ile Glu Glu Ser Glu Ser Thr Glu Thr Thr Gly Val Ala Phe  
 465 470 475 480  
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 Asp His Gln Ala Pro Leu Thr Thr Ser Glu Ile Lys Leu Lys Met Asn  
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Ser Arg Val Val Gly Gly Ile Met Thr Gly Glu Lys Lys Asp Gly Phe  
515 520 525

Ser Asp Pro Ile Ile Tyr Thr Leu Glu Asn Val Gln Pro Lys Gln Lys  
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Phe Glu Arg Pro Ile Cys Val Ser Trp Ser Thr Asp Val Lys Gly Gly  
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Arg Trp Thr Ser Phe Gly Cys Val Ile Leu Glu Ala Ser Glu Thr Tyr  
565 570 575

Thr Ile Cys Ser Cys Asn Gln Met Ala Asn Leu Ala Val Ile Met Ala  
580 585 590

Ser Gly Glu Leu Thr Met Asp Phe Ser Leu Tyr Ile Ile Ser His Val  
595 600 605

Gly Ile Ile Ile Ser Leu Val Cys Leu Val Leu Ala Ile Ala Thr Phe  
610 615 620

Leu Leu Cys Arg Ser Ile Arg Asn His Asn Thr Tyr Leu His Leu His  
625 630 635 640

Leu Cys Val Cys Leu Leu Leu Ala Lys Thr Leu Phe Leu Ala Gly Ile  
645 650 655

His Lys Thr Asp Asn Lys Thr Gly Cys Ala Ile Ile Ala Gly Phe Leu  
660 665 670

His Tyr Leu Phe Leu Ala Cys Phe Phe Trp Met Leu Val Glu Ala Val  
675 680 685

Ile Leu Phe Leu Met Val Arg Asn Leu Lys Val Val Asn Tyr Phe Ser  
690 695 700

Ser Arg Asn Ile Lys Met Leu His Ile Cys Ala Phe Gly Tyr Gly Leu  
705 710 715 720

Pro Met Leu Val Val Val Ile Ser Ala Ser Val Gln Pro Gln Gly Tyr  
725 730 735

Gly Met His Asn Arg Cys Trp Leu Asn Thr Glu Thr Gly Phe Ile Trp  
740 745 750

Ser Phe Leu Gly Pro Val Cys Thr Val Ile Val Ile Asn Ser Leu Leu  
755 760 765

Leu Thr Trp Thr Leu Trp Ile Leu Arg Gln Arg Leu Ser Ser Val Asn  
770 775 780

Ala Glu Val Ser Thr Leu Lys Asp Thr Arg Leu Leu Thr Phe Lys Ala  
785 790 795 800

Phe Ala Gln Leu Phe Ile Leu Gly Cys Ser Trp Val Leu Gly Ile Phe



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Leu Gly Ser Tyr Tyr Cys Thr Cys Asn Ser Gly Leu Glu Ser Ser Gly		
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Glu Cys Ser Arg Asn Ser Thr Leu Cys Gly Pro Thr Phe Ile Cys Ile		
225	230	235
Asn Thr Leu Gly Ser Tyr Ser Cys Ser Cys Pro Ala Gly Phe Ser Leu		
245	250	255
Pro Thr Phe Gln Ile Leu Gly His Pro Ala Asp Gly Asn Cys Thr Asp		
260	265	270
Ile Asp Glu Cys Asp Asp Thr Cys Pro Leu Asn Ser Ser Cys Thr Asn		
275	280	285
Thr Ile Gly Ser Tyr Phe Cys Thr Cys His Pro Gly Phe Ala Ser Ser		
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Asn Gly Gln Leu Asn Phe Lys Asp Leu Glu Val Thr Cys Glu Asp Ile		
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Asp Glu Cys Thr Gln Asp Pro Leu Gln Cys Gly Leu Asn Ser Val Cys		
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Thr Asn Val Pro Gly Ser Tyr Ile Cys Gly Cys Leu Pro Asp Phe Gln		
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Met Asp Pro Glu Gly Ser Gln Gly Tyr Gly Asn Phe Asn Cys Lys Arg		
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Ile Leu Phe Lys Cys Lys Glu Asp Leu Ile Leu Gln Ser Glu Gln Ile		
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Gln Gln Cys Gln Ala Val Gln Gly Arg Asp Leu Gly Tyr Ala Ser Phe		
385	390	395
Cys Thr Leu Val Asn Ala Thr Phe Thr Ile Leu Asp Asn Thr Cys Glu		
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Asn Lys Ser Ala Pro Val Ser Leu Gln Ser Ala Ala Thr Ser Val Ser		
420	425	430
Leu Val Leu Glu Gln Ala Thr Thr Trp Phe Glu Leu Ser Lys Glu Glu		
435	440	445
Thr Ser Thr Leu Gly Thr Ile Leu Leu Glu Thr Val Glu Ser Thr Met		
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Glu	Asn	Glu	Ser	Ile	Asn	Leu	Ala	Ala	Arg	Gly	Asp	Lys	Met	Asn	Val	500	505	510	
Gly	Cys	Phe	Ile	Ile	Lys	Glu	Ser	Val	Ser	Thr	Gly	Ala	Pro	Gly	Val	515	520	525	
Ala	Phe	Val	Ser	Phe	Ala	His	Met	Glu	Ser	Val	Leu	Asn	Glu	Arg	Phe	530	535	540	
Phe	Glu	Asp	Gly	Gln	Ser	Phe	Arg	Lys	Leu	Arg	Met	Asn	Ser	Arg	Val	545	550	555	560
Val	Gly	Gly	Thr	Val	Thr	Gly	Glu	Lys	Lys	Glu	Asp	Phe	Ser	Lys	Pro	565	570	575	
Ile	Ile	Tyr	Thr	Leu	Gln	His	Ile	Gln	Pro	Lys	Gln	Lys	Ser	Glu	Arg	580	585	590	
Pro	Ile	Cys	Val	Ser	Trp	Asn	Thr	Asp	Val	Glu	Asp	Gly	Arg	Trp	Thr	595	600	605	
Pro	Ser	Gly	Cys	Glu	Ile	Val	Glu	Ala	Ser	Glu	Thr	His	Thr	Val	Cys	610	615	620	
Ser	Cys	Asn	Arg	Met	Ala	Asn	Leu	Ala	Ile	Ile	Met	Ala	Ser	Gly	Glu	625	630	635	640
Leu	Thr	Met	Glu	Phe	Ser	Leu	Tyr	Ile	Ile	Ser	His	Val	Gly	Thr	Val	645	650	655	
Ile	Ser	Leu	Val	Cys	Leu	Ala	Leu	Ala	Ile	Ala	Thr	Phe	Leu	Leu	Cys	660	665	670	
Arg	Ala	Val	Gln	Asn	His	Asn	Thr	Tyr	Met	His	Leu	His	Leu	Cys	Val	675	680	685	
Cys	Leu	Phe	Leu	Ala	Lys	Ile	Leu	Phe	Leu	Thr	Gly	Ile	Asp	Lys	Thr	690	695	700	
Asp	Asn	Gln	Thr	Ala	Cys	Ala	Ile	Ile	Ala	Gly	Phe	Leu	His	Tyr	Leu	705	710	715	720
Phe	Leu	Ala	Cys	Phe	Phe	Trp	Met	Leu	Val	Glu	Ala	Val	Met	Leu	Phe	725	730	735	
Leu	Met	Val	Arg	Asn	Leu	Lys	Val	Val	Asn	Tyr	Phe	Ser	Ser	Arg	Asn	740	745	750	

Ile Lys Met Leu His Leu Cys Ala Phe Gly Tyr Gly Leu Pro Val Leu  
755 760 765

Val Val Ile Ile Ser Ala Ser Val Gln Pro Arg Gly Tyr Gly Met His  
770 775 780

Asn Arg Cys Trp Leu Asn Thr Glu Thr Gly Phe Ile Trp Ser Phe Leu  
785 790 795 800

Gly Pro Val Cys Met Ile Ile Thr Ile Asn Ser Val Leu Leu Ala Trp  
805 810 815

Thr Leu Trp Val Leu Arg Gln Lys Leu Cys Ser Val Ser Ser Glu Val  
820 825 830

Ser Lys Leu Lys Asp Thr Arg Leu Leu Thr Phe Lys Ala Ile Ala Gln  
835 840 845

Ile Phe Ile Leu Gly Cys Ser Trp Val Leu Gly Ile Phe Gln Ile Gly  
850 855 860

Pro Leu Ala Ser Ile Met Ala Tyr Leu Phe Thr Ile Ile Asn Ser Leu  
865 870 875 880

Gln Gly Ala Phe Ile Phe Leu Ile His Cys Leu Leu Asn Arg Gln Val  
885 890 895

Arg Asp Glu Tyr Lys Lys Leu Leu Thr Arg Lys Thr Asp Leu Ser Ser  
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Ser Ser Phe Ser Glu Ile Ile Thr Thr Pro Thr Glu Thr Cys Asp Asp  
50 55 60

Albuquerque, New Mexico



355	360	365
Phe Ala Phe Ser His Leu Glu Ser Ser Asp Gly Glu Ala Gly Arg Asp		
370	375	380
Pro Pro Ala Lys Asp Val Met Pro Gly Pro Arg Gln Glu Leu Leu Cys		
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Ser His Leu Ser Ser Phe Thr Ile Leu Met Ala His Tyr Asp Val Glu		
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Asp Trp Lys Leu Thr Leu Ile Thr Arg Val Gly Leu Ala Leu Ser Leu		
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Phe Cys Leu Leu Leu Cys Ile Leu Thr Phe Leu Leu Val Arg Pro Ile		
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Gln Gly Ser Arg Thr Thr Ile His Leu His Leu Cys Ile Cys Leu Phe		
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Val Gly Ser Thr Ile Phe Leu Ala Gly Ile Glu Asn Glu Gly Gly Gln		
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Val Gly Leu Arg Cys Arg Leu Val Ala Gly Leu Leu His Tyr Cys Phe		
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Leu Ala Ala Phe Cys Trp Met Ser Leu Glu Gly Leu Glu Leu Tyr Phe		
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Leu Val Val Arg Val Phe Gln Gly Gln Gly Leu Ser Thr Arg Trp Leu		
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Ala Ile Tyr Ser Lys Gly Tyr Gly Arg Pro Arg Tyr Cys Trp Leu Asp		
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	595	600 605
Ile Leu Cys Asn Ala Val Ile Phe Val Thr Thr Val Trp Lys Leu Thr		
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Gln Lys Phe Ser Glu Ile Asn Pro Asp Met Lys Lys Leu Lys Lys Ala		
625	630	635 640
Arg Ala Leu Thr Ile Thr Ala Ile Ala Gln Leu Phe Leu Leu Gly Cys		
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Thr Trp Val Phe Gly Leu Phe Ile Phe Asp Asp Arg Ser Leu Val Leu  
 660 665 670

Thr Tyr Val Phe Thr Ile Leu Asn Cys Leu Gln Gly Ala Phe Leu Tyr  
 675 680 685

Leu Leu His Cys Leu Leu Asn Lys Lys Val Arg Glu Glu Tyr Arg Lys  
 690 695 700

Trp Ala Cys Leu Val Ala Gly Gly Ser Lys Tyr Ser Glu Phe Thr Ser  
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<210> 9  
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<210> 17  
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<400> 17  
gaaagtttgc ttctcaaaat cca 23

<210> 18  
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<400> 19  
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<210> 20  
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<210> 21

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<210> 23  
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<400> 25

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SEQUENCE LISTING

<110> CAMINSCHI ET AL.

<120> DENDRITIC CELL MEMBRANE PROTEIN FIRE

<130> FBRC:011US

<140> 10/070,982

<141> 2002-03-08

<150> PCT/AU00/01083

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<170> PatentIn Ver. 2.1

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<213> Mus musculus

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Cys Asn Glu Asn Ala Ser Cys Phe Asn Ser Thr His Cys Val Cys Lys  
35 40 45

Glu Gly Phe Trp Thr Gly Ser Glu Asn Arg Arg Ile Ile Glu Pro His  
50 55 60

Glu Lys Cys Gln Asp Ile Asn Glu Cys Leu Leu Lys Glu Leu Val Cys  
65 70 75 80

Lys Asp Val Ser Tyr Cys Arg Asn Lys Ile Gly Thr Tyr Ile Cys Ser  
85 90 95

Cys Val Val Lys Tyr Pro Leu Phe Asn Trp Val Ala Gly Ile Ile Asn  
100 105 110

Ile Asp His Pro Asp Cys Tyr Val Asn Lys Ser Lys Asn Thr Gly Ser  
115 120 125

Lys Thr His Thr Leu Gly Val Leu Ser Glu Phe Lys Ser Lys Glu Glu  
130 135 140

Val Ala Lys Gly Ala Thr Lys Leu Leu Arg Lys Val Glu His His Ile  
145 150 155 160

Leu Asn Glu Asn Ser Asp Ile Pro Lys Lys Asp Glu Asn Pro Leu Leu  
165 170 175







Gly	Tyr	Ile	Cys	Ser	Cys	Leu	Val	Lys	Tyr	Thr	Leu	Phe	Asn	Phe	Leu	65	70	75	80
Ala	Gly	Ile	Ile	Asp	Tyr	Asp	His	Pro	Asp	Cys	Tyr	Glu	Asn	Asn	Ser	85	90	95	
Gln	Gly	Thr	Thr	Gln	Ser	Asn	Val	Asp	Ile	Trp	Glu	Asn	Leu	Arg	Arg	100	105	110	
Asn	Gly	Ser	Arg	Glu	Asp	Phe	Ala	Arg	Arg	Ala	Thr	Gln	Leu	Ile	Gln	115	120	125	
Ser	Val	Glu	Leu	Ser	Ile	Trp	Asn	Ala	Ser	Phe	Ala	Ser	Pro	Gly	Lys	130	135	140	
Gly	Gln	Ile	Ser	Glu	Phe	Asp	Ile	Val	Tyr	Glu	Thr	Lys	Arg	Cys	Asn	145	150	155	160
Glu	Thr	Arg	Glu	Asn	Ala	Phe	Leu	Glu	Ala	Gly	Asn	Asn	Thr	Met	Asp	165	170	175	
Ile	Asn	Cys	Ala	Asp	Ala	Leu	Lys	Gly	Asn	Leu	Arg	Glu	Ser	Thr	Ala	180	185	190	
Val	Ala	Leu	Ile	Thr	Tyr	Gln	Ser	Leu	Gly	Asp	Ile	Leu	Asn	Ala	Ser	195	200	205	
Phe	Phe	Ser	Lys	Arg	Lys	Gly	Met	Gln	Glu	Val	Lys	Leu	Asn	Ser	Tyr	210	215	220	
Val	Val	Ser	Gly	Thr	Val	Gly	Leu	Lys	Glu	Lys	Ile	Ser	Leu	Ser	Glu	225	230	235	240
Pro	Val	Phe	Leu	Thr	Phe	Arg	His	Asn	Gln	Pro	Gly	Asp	Lys	Arg	Thr	245	250	255	
Lys	His	Ile	Cys	Val	Tyr	Trp	Glu	Gly	Ser	Glu	Gly	Gly	Arg	Trp	Ser	260	265	270	
Thr	Glu	Gly	Cys	Ser	His	Val	His	Ser	Asn	Gly	Ser	Tyr	Thr	Lys	Cys	275	280	285	
Lys	Cys	Phe	His	Leu	Ser	Ser	Phe	Ala	Val	Leu	Val	Ala	Leu	Ala	Pro	290	295	300	
Lys	Glu	Asp	Pro	Val	Leu	Thr	Val	Ile	Thr	Gln	Val	Gly	Leu	Thr	Ile	305	310	315	320
Ser	Leu	Leu	Cys	Leu	Phe	Leu	Ala	Ile	Leu	Thr	Phe	Leu	Leu	Cys	Arg	325	330	335	
Pro	Ile	Gln	Asn	Thr	Ser	Thr	Ser	Leu	His	Leu	Glu	Leu	Ser	Leu	Cys	340	345	350	
Leu	Phe	Leu	Ala	His	Leu	Leu	Phe	Leu	Thr	Gly	Ile	Asn	Arg	Thr	Glu	355	360	365	

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Leu Ala Cys Phe Thr Trp Met Leu Leu Glu Gly Leu His Leu Phe Leu  
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Lys Lys Arg Phe Met Tyr Pro Val Gly Tyr Gly Ile Pro Ala Val Ile  
420 425 430

His Cys Trp Leu Lys Leu Asp Lys Gly Phe Ile Trp Ser Phe Met Gly  
450 455 460

Leu Trp Ile Leu Arg Ser Lys Leu Ser Ser Leu Asn Lys Glu Val Ser  
485 490 495

Phe Ile Leu Gly Cys Ser Trp Gly Leu Gly Phe Phe Met Val Glu Glu  
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Val Gly Lys Thr Ile Gly Ser Ile Ile Ala Tyr Ser Phe Thr Ile Ile  
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Asn Thr Leu Gln Gly Val Leu Leu Phe Val Val His Cys Leu Leu Asn  
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Arg Gln Val Arg Met Glu Tyr Lys Lys Trp Phe Ser Gly Met Arg Lys  
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Lys Thr Glu Glu Val Gly Lys Ser Ser Glu Ile Phe His Lys Gly Gly  
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His Leu Val Ser Ala Ala Trp Leu Lys Met Asn  
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<212> DNA

<213> Mus musculus

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ctgcttcaac agcaccact gtgtttgtaa agaaggattc tggacgggct ctgagaatag 300
aagaattatt gagcccatg agaaatgtca agatattaat gagtgtctac tgaagaatt 360
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3258

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 <213> Homo sapiens

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<211> 886

<212> PRT

<213> Homo sapiens

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35 40 45

Asn Thr Val Asp Ser Tyr Tyr Cys Thr Cys Lys Gln Gly Phe Leu Ser  
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Ser Asn Gly Gln Asn His Phe Lys Asp Pro Gly Val Arg Cys Lys Asp  
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Ile Asp Glu Cys Ser Gln Ser Pro Gln Pro Cys Gly Pro Asn Ser Ser  
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Cys Lys Asn Leu Ser Gly Arg Tyr Lys Cys Ser Cys Leu Asp Gly Phe  
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Ser Ser Pro Thr Gly Asn Asp Trp Val Pro Gly Lys Pro Gly Asn Phe  
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Ser Cys Thr Asp Ile Asn Glu Cys Leu Thr Ser Arg Val Cys Pro Glu  
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His Ser Asp Cys Val Asn Ser Met Gly Ser Tyr Ser Cys Ser Cys Gln  
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Val Gly Phe Ile Ser Arg Asn Ser Thr Cys Glu Asp Val Asn Glu Cys  
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Ala Asp Pro Arg Ala Cys Pro Glu His Ala Thr Cys Asn Asn Thr Val  
180 185 190

Gly Asn Tyr Ser Cys Phe Cys Asn Pro Gly Phe Glu Ser Ser Ser Gly  
195 200 205

His Leu Ser Cys Gln Gly Leu Lys Ala Ser Cys Glu Asp Ile Asp Glu  
210 215 220

Cys Thr Glu Met Cys Pro Ile Asn Ser Thr Cys Thr Asn Thr Pro Gly  
225 230 235 240

Ser Tyr Phe Cys Thr Cys His Pro Gly Phe Ala Pro Ser Ser Gly Gln  
245 250 255

Leu Asn Phe Thr Asp Gln Gly Val Glu Cys Arg Asp Ile Asp Glu Cys  
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Arg Gln Asp Pro Ser Thr Cys Gly Pro Asn Ser Ile Cys Thr Asn Ala

275	280	285
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Glu Gly Ser Gln Lys Asp Gly Asn Phe Ser Cys Gln Arg Val Leu Phe 305 310 315 320		
Lys Cys Lys Glu Asp Val Ile Pro Asp Asn Lys Gln Ile Gln Gln Cys 325 330 335		
Gln Glu Gly Thr Ala Val Lys Pro Ala Tyr Val Ser Phe Cys Ala Gln 340 345 350		
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885

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Phe	Leu	Cys	Ala	Asp	Val	Asp	Glu	Cys	Leu	Thr	Ile	Gly	Ile	Cys	Pro	
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 595 600 605  
 Pro Ser Gly Cys Glu Ile Val Glu Ala Ser Glu Thr His Thr Val Cys  
 610 615 620  
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 625 630 635 640  
 Leu Thr Met Glu Phe Ser Leu Tyr Ile Ile Ser His Val Gly Thr Val  
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 Gly Pro Val Cys Met Ile Ile Thr Ile Asn Ser Val Leu Leu Ala Trp  
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 Thr Leu Trp Val Leu Arg Gln Lys Leu Cys Ser Val Ser Ser Glu Val  
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[illegible]

8 6

34

<213> Artificial Sequence

<223> Description of Artificial Sequence: PCR primers

31

<213> Artificial Sequence

<223> Description of Artificial Sequence: PCR primers

32

<213> Mus musculus

20

<213> Mus musculus

23

<213> Homo sapiens

26



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<212> DNA  
<213> Homo sapiens

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19

<210> 20  
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<212> DNA  
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33

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33

<210> 22  
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33

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<212> DNA
<213> Artificial Sequence
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<400> 25  
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